Temperature affects chemical defense in a mite-beetle predator-prey system

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Supplementary Text S1 – detailed equations

The chemical defense dynamic and functional response models can be formalized (Heethoff and Rall 2015) by describing the number of prey individuals – either chemically defended or undefended – attacked (and eaten) by a predator as:

$$\frac{dN}{dt} = -F \quad (1a)$$

$$\frac{dS}{dt} = P_S - e_S \frac{F_S}{N} \quad (1b)$$

where N (N A^{-1}_{area}) is the change of prey individual density (eq. **1a**), S (ng N^{-1}) is the change of per capita defensive secretions (eq. **1b**) over t (h) time, F (N h^{-1}) is the functional response of undefended and F_S (N_S h^{-1}) is the function response of defended mites. Furthermore e_s (ng N^{-1}) and P_s (ng $N^{-1}h^{-1}$) are factors describing the amount of defensive secretion lost per attack and the per capita secretion production over time, respectively.

To model the functional response, Heethoff and Rall (2015) chose a traditional type II functional response in habitat-free foraging space (Holling 1959; Vucic-Pestic et al. 2010) and extended the classic equation resulting in two new models; F for undefended mites (eq. **2a**) and F_S for defended (eq. **2b**):

$$F = \frac{\sigma\alpha(N - N_S)}{1 + \sigma\alpha T_h(N - N_S) + (1 - \sigma)\alpha T_U(N - N_S) + \alpha T_U N_S} \quad (2a)$$

$$F_S = \frac{\alpha N_S}{1 + \sigma\alpha T_h(N - N_S) + (1 - \sigma)\alpha T_U(N - N_S) + \alpha T_U N_S} \quad (2b)$$

where T_h (h N^{-1}) is the handling time, α (A_{area} h^{-1}) is the attack rate, σ is the success rate and T_U (h) is the time needed/wasted for failed attacks.

The gross change of the per capita secretion rate over time (S_t) without any disturbance from predators (eq. **1b** with F_S= 0) can be written as [eq. **3,** Heethoff and Rall (2015)]:

$$S_t = \frac{-K_S + K_s e^{\frac{R_S t}{K_S}} + S_{t=0}}{e^{\frac{R_S t}{K_S}}} \quad (3)$$

with K_S (ng N^{-1}) as the reservoir size and R_S (ng h^{-1} N^{-1}) as the regeneration rate of a subpopulation of defended prey. This assumes, that the regeneration of the defensive secretions starts immediately after a depletion event and until the maximum reservoir filling under given circumstances are reached. Both sides of eq. **3** can be $\log_{10}$-transformed to ensure normality of the model residuals. Consequently, eq. **3** can be used to fit experimentally measured quantitative secretion data over time to estimate K_S and R_S for different treatments after total depletion of the glandular contents (e.g. by artificial stimuli; Heethoff and Raspotnig (2012)). Both parameters are used to describe the *per capita* secretion production over time P_S (eq. **4**) to finally model the system with the two ordinary differential equations (eq. **1a** and eq. **1b**) but see Heethoff and Rall (2015) for further details.

$$P_S = R_S\left(1 - \frac{S}{K_S}\right) \quad (4)$$

To model the survival of prey, K_S (ng N^{-1}) and R_S (ng h^{-1} N^{-1}) were subsequently used together with the discovery rate α (A_{area} h^{-1}) and handling times T_h (h N^{-1}) for model parametrization, thereby α (A_{area} h^{-1}) and T_h (h N^{-1}) were calculated according to Binzer et al. (2012) and Rall et al. (2012) based on a predator mass of 3.5 mg (corresponding to the rove beetle *Stenus juno*, a model predator of oribatid mites, Heethoff et al. 2011) and measured prey body masses m_{mite} (µg) (mean for each temperature, see supplementary material). The rate of successful attacks σ in case of undefended prey was set to 0.28 and the amount of defensive secretion lost per attack e_s to 50 ng N^{-1} based on empirical data from Heethoff et al. (2011) as well as Raspotnig (2006) and Heethoff (2012), respectively.

As we were interested in the number of prey specimens surviving because of chemical defense at a given temperature, we used eq. **5** (for more details see Brückner and Heethoff 2018) to extract this information from the simulated data. The calculated (eq. **5**) effective chemical defense is therefore the number of surviving mite individuals caused by chemical defense Δ_{chem} (N A_{area}^{-1}) at a given time:

$$\Delta_{chem} = N_{S,t_n} - N_{t_n} \quad (5)$$

where N_{S,t_n} (N A_{area}^{-1}) is the number of living, defended mites at a given time (i.e. model including chemical defense and other parameters like body mass) and N_{t_n} (N A_{area}^{-1}) is the number of living, undefended mites at a given time (i.e. the null-model excluding chemical defense, but including other parameters e.g., body mass differences). Finally, we simulated both scenarios (eq. **1a** and eq. **1b)** and calculate the effective chemical defense Δ_{chem} (eq. **5**) over time at the different temperature regimes using the generic lsoda()-function in R (R Core

R_Core_Team 2019) with a total number of 100 prey individuals and a time step length of 0.1 h (n_{steps}= 1,000).

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